

100701-0002001

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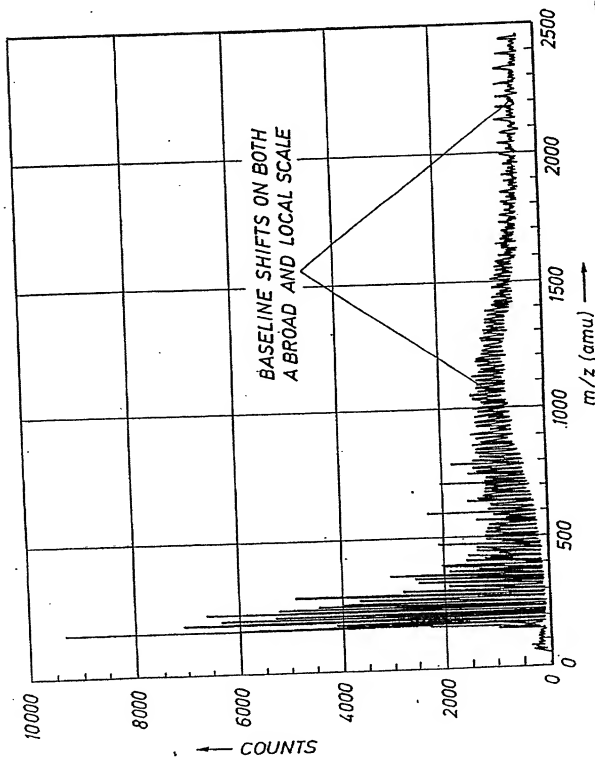


FIG. 1

+

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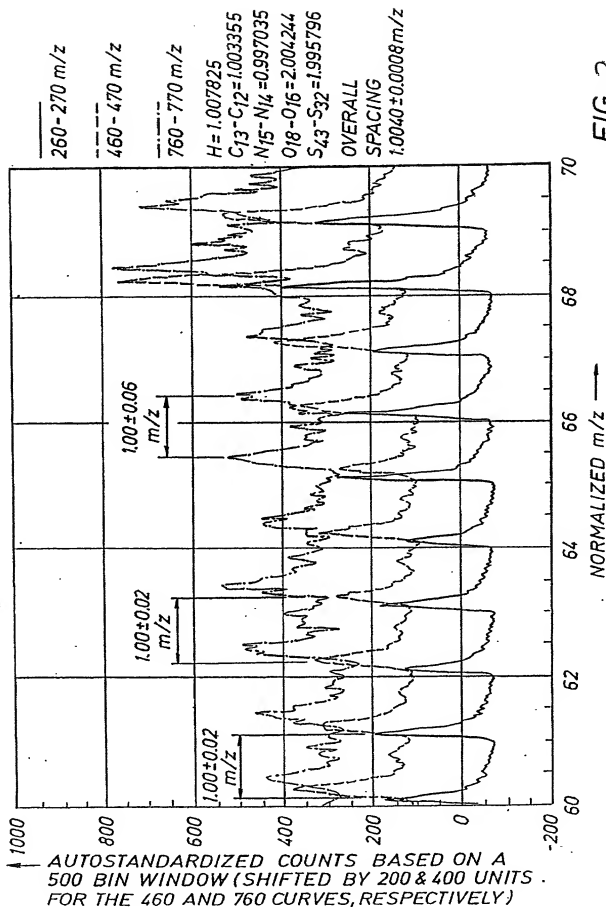


FIG. 2

+

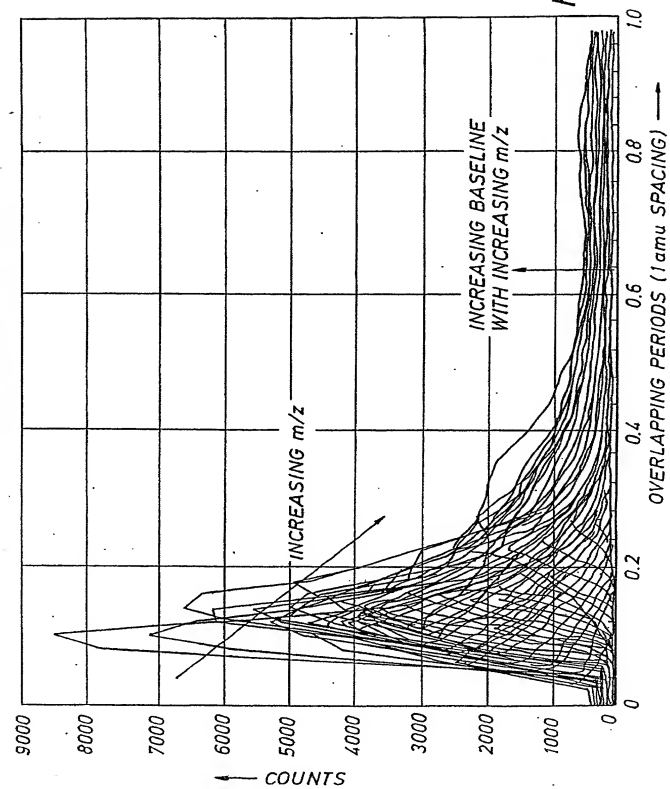


FIG. 3

106101-20222001

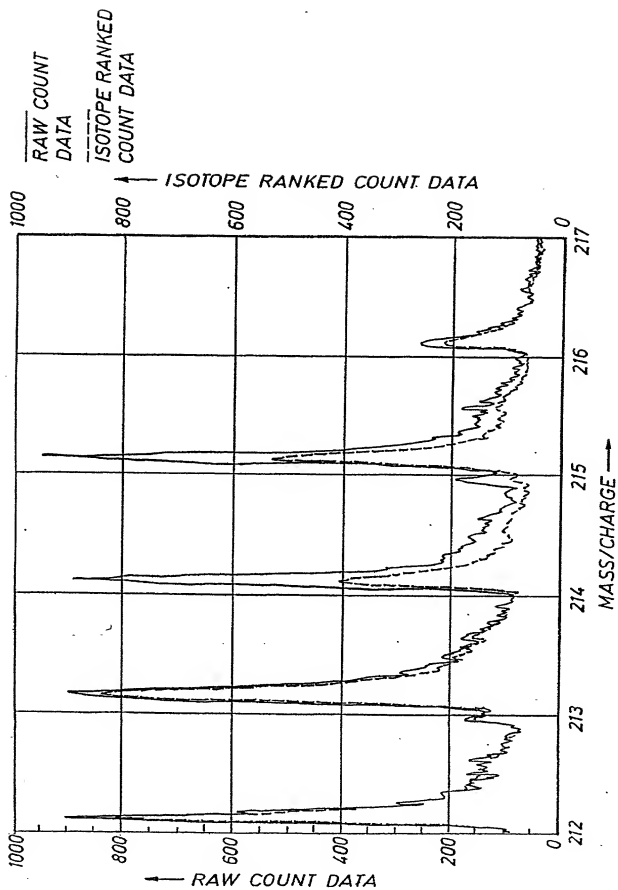


Fig. 4

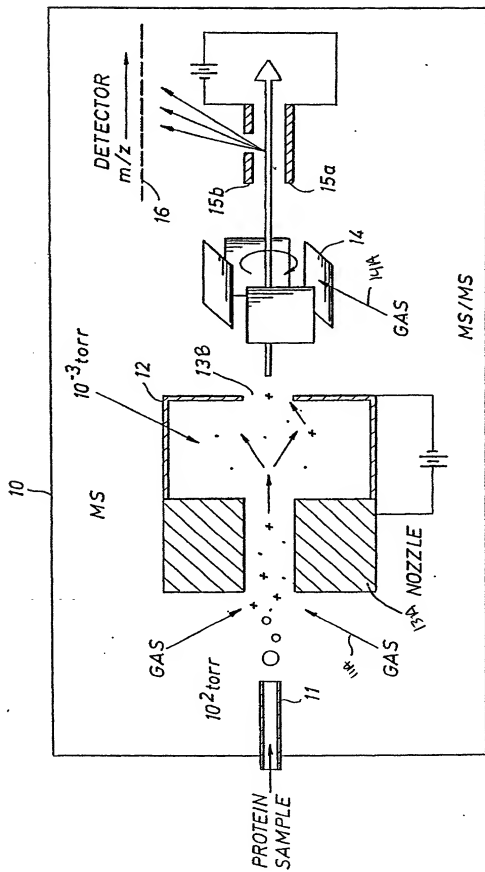


FIG. 5

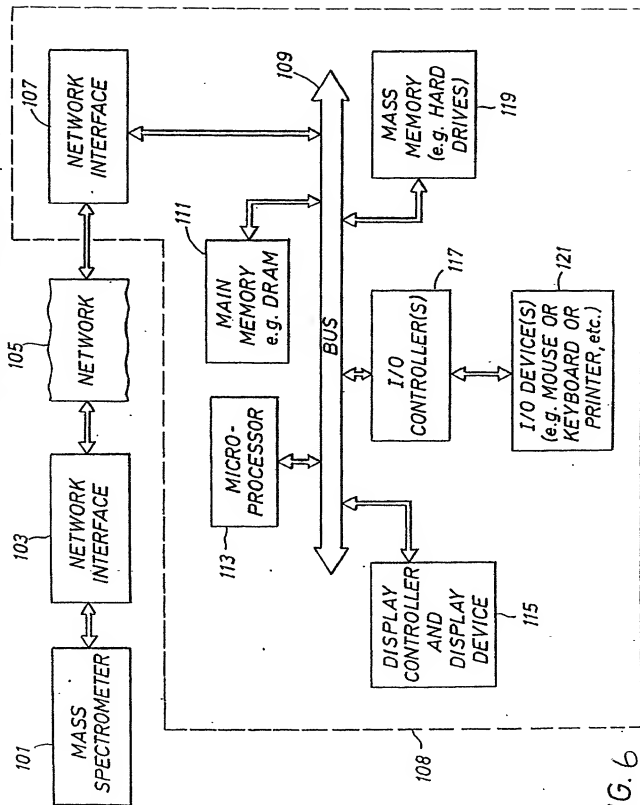


FIG. 6

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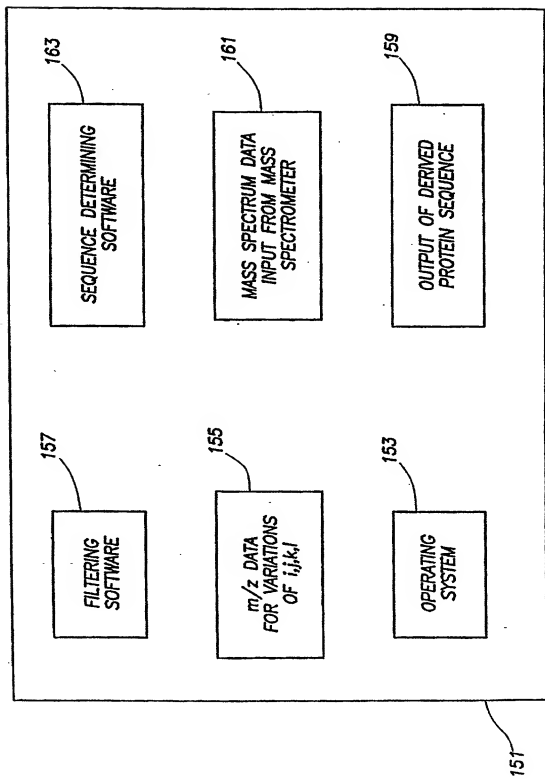
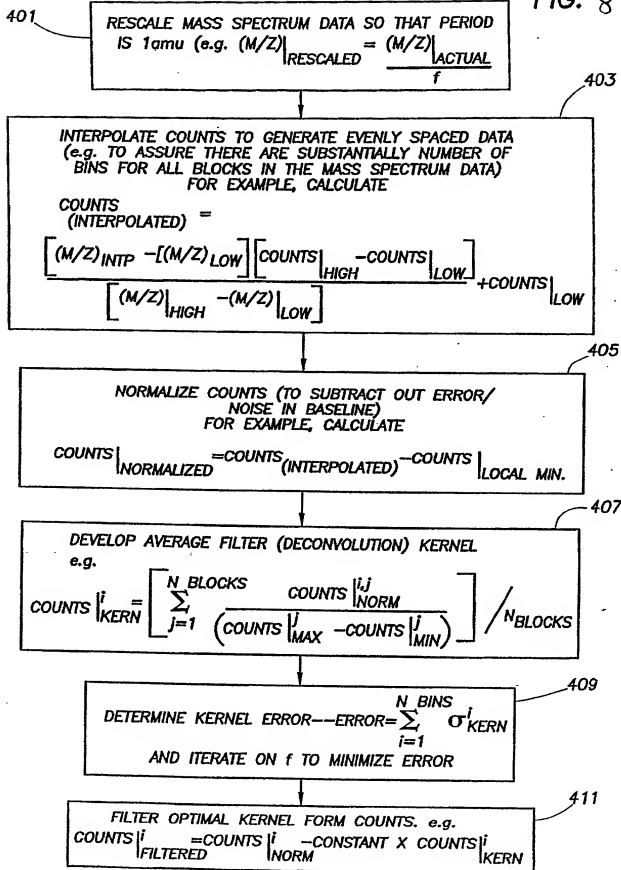


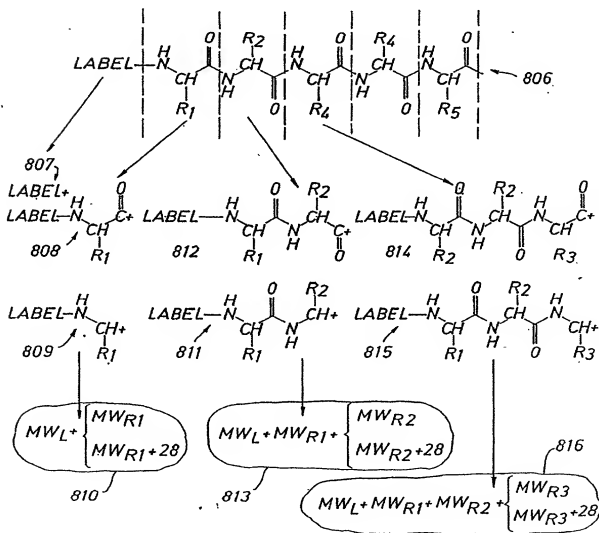
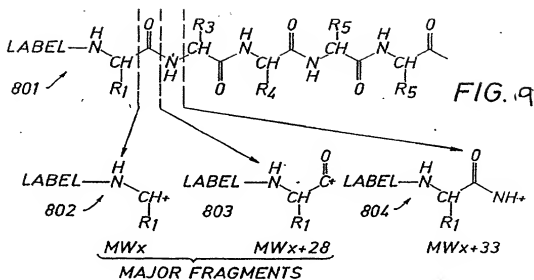
FIG. 7

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FIG. 8



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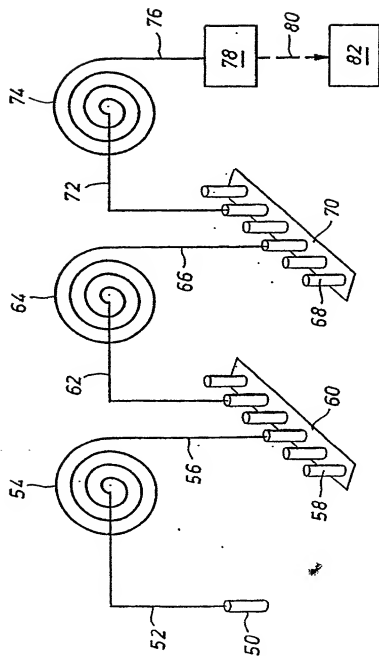


FIG. 10

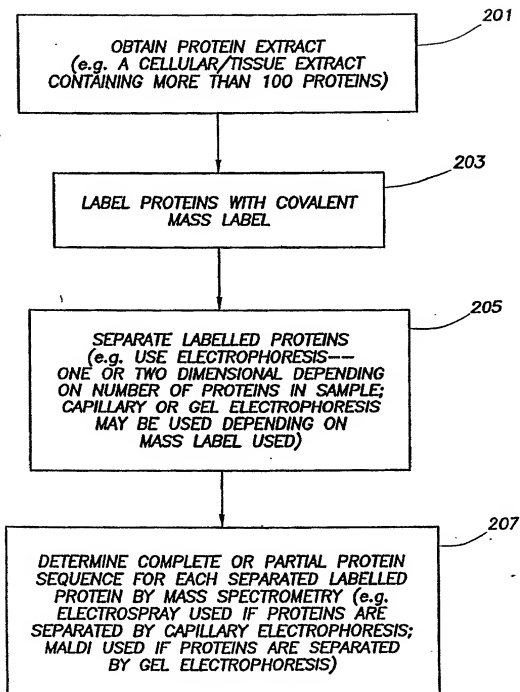


FIG. 11

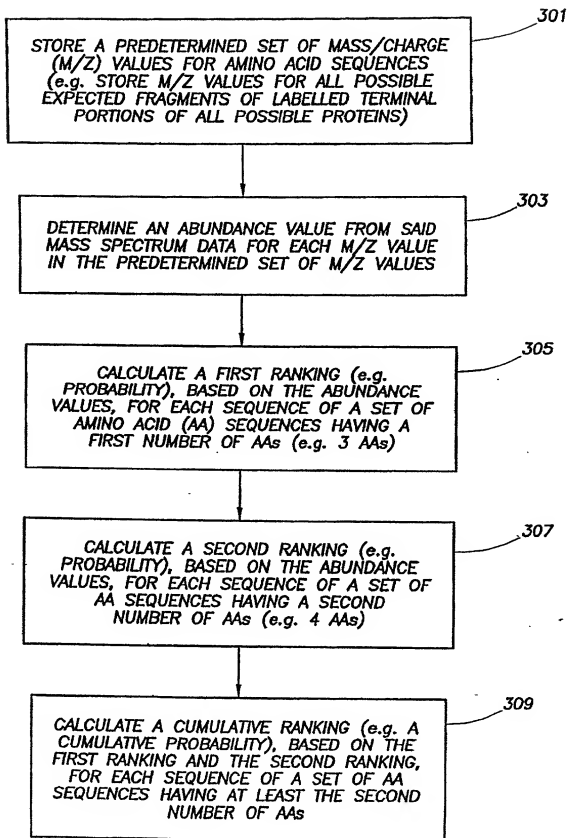


FIG. 13

FIG. 14A

FOR EACH POSSIBLE EXPECTED FRAGMENT OF A TERMINALLY LABELLED SEQUENCE OF AAs, PERFORM LOOKUP IN MASS SPECTRUM DATA FOR ABUNDANCE VALUE AT M/Z VALUE OF POSSIBLE EXPECTED FRAGMENT (e.g. $C_{i,j,k,l} = \text{LOOKUP} [(M/Z)_{i,j,k,l}]$)

DETERMINE MASTER COUNT, FOR EACH PARTICULAR POSSIBLE SEQUENCE, OVER ALL POSSIBLE ION TYPES AND CHARGE STATES FOR PARTICULAR SEQUENCE

e.g.

$$C_{i,j}^M = \sum_{l=\text{MIN CHARGE STATES}}^{\text{MAX CHARGE STATES}} \left(\sum_{k=1}^{\text{MAX ION TYPES}} C_{i,j,k,l} \right)$$

WHERE

i =NUMBER OF AMINO ACIDS (AAs) IN SEQUENCE
 j =NUMBER OF POSSIBLE SEQUENCES (USUALLY, 19)
 l =NUMBER OF ION TYPES FOR EACH RESIDUE (e.g. ION TYPES a,b, AND POSSIBLY c AT N TERMINUS AND ION TYPES x,y, AND POSSIBLY z AT C TERMINUS)
 k =NUMBER OF CHARGE STATES FOR EACH ION TYPE

FOR EACH MASTER COUNT ($C_{i,j}^M$) FOR A PARTICULAR POSSIBLE SEQUENCE AT A GIVEN SEQUENCE LENGTH, COMPARE THE MASTER COUNT TO ALL OTHER MASTER COUNTS FOR ALL OTHER POSSIBLE SEQUENCES FOR THE GIVEN SEQUENCE LENGTH TO PRODUCE A RANKING OF MASTER COUNTS OF ALL POSSIBLE SEQUENCES AT THE GIVEN LENGTH OF AAs. FOR EXAMPLE, THE COMPARISON MAY BE A RANKING OF PROBABILITIES WHERE EACH PROBABILITY IS A PROBABILITY OF A PARTICULAR SEQUENCE AT THE GIVEN SEQUENCE LENGTH RELATIVE TO ALL OTHER POSSIBLE SEQUENCES AT THE SAME LENGTH

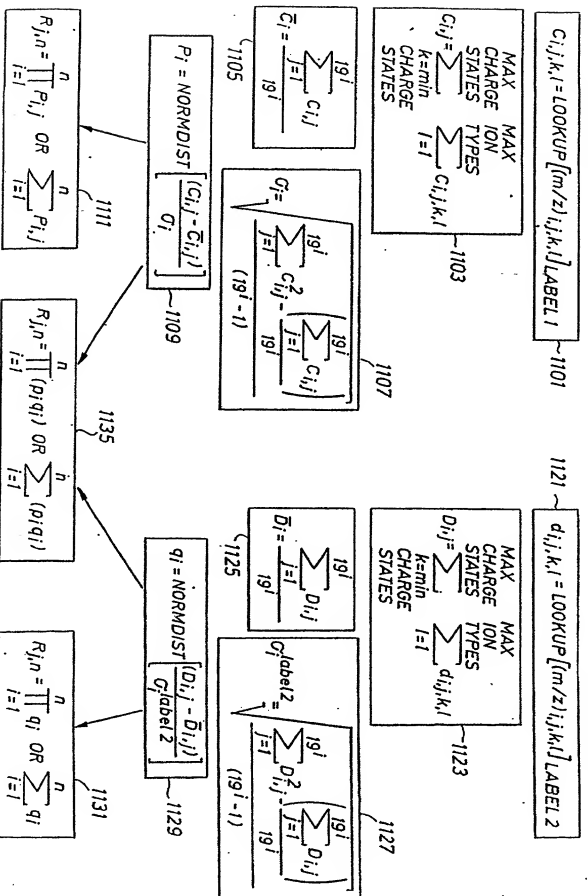
TO FIG. 14B

[illegible]

LABEL 1

FIG. 15

LABEL 2



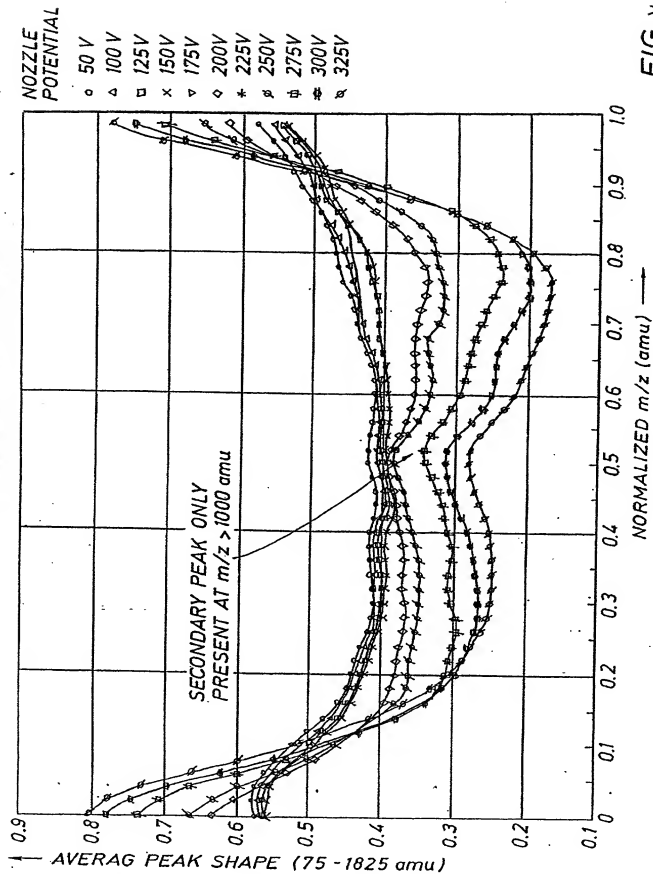


FIG. 16

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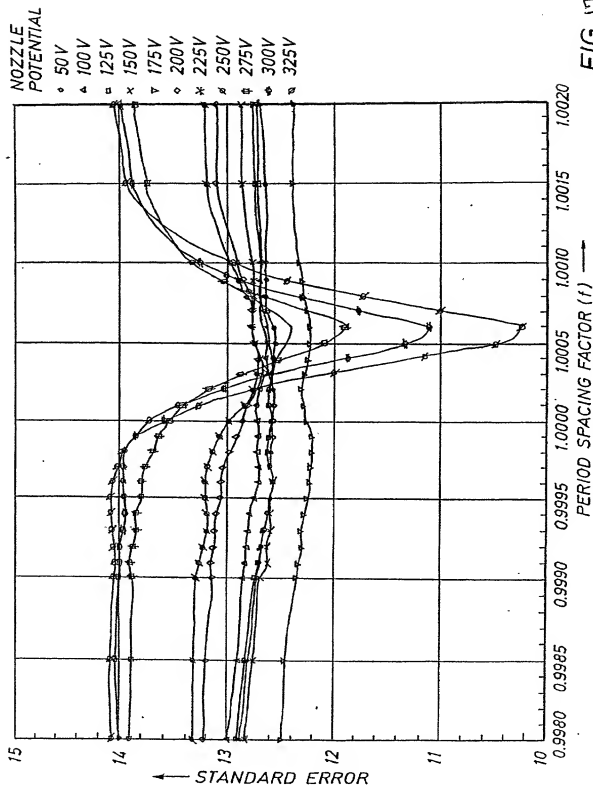
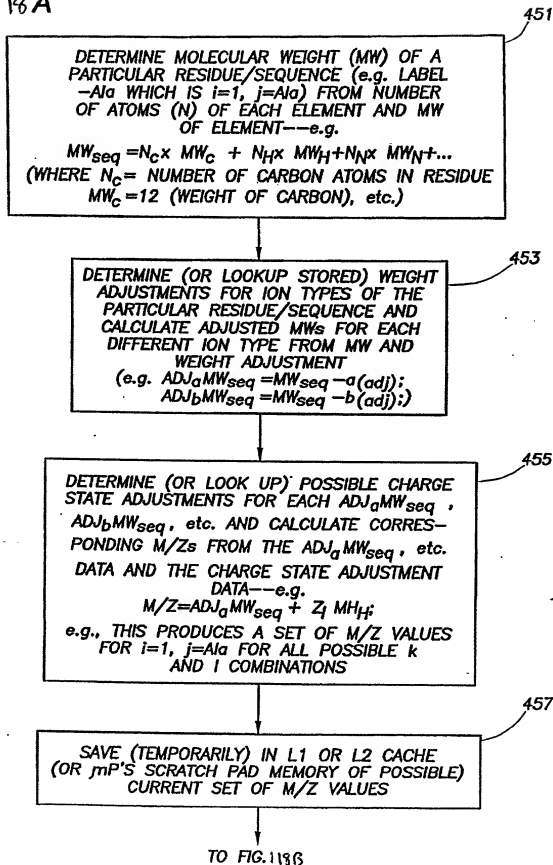


FIG. 17

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FIG. 18'A



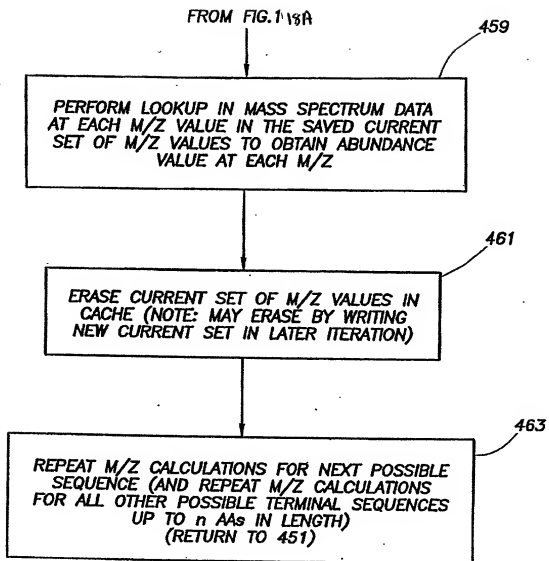


FIG. 118B

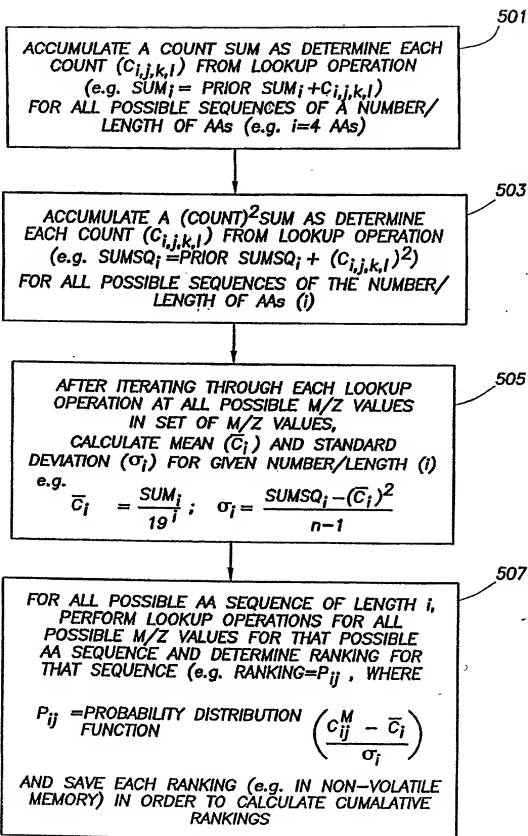


FIG. 19

FIG. 20A

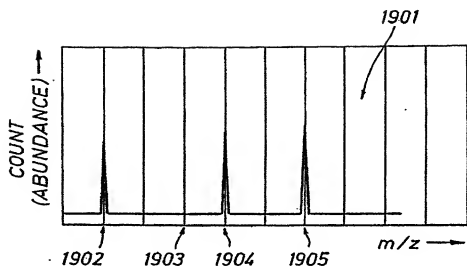
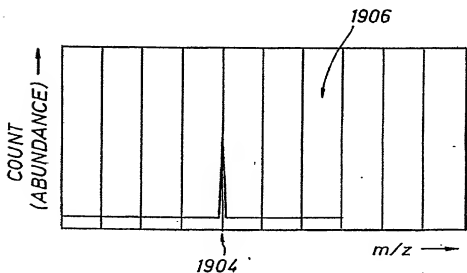


FIG. 20B



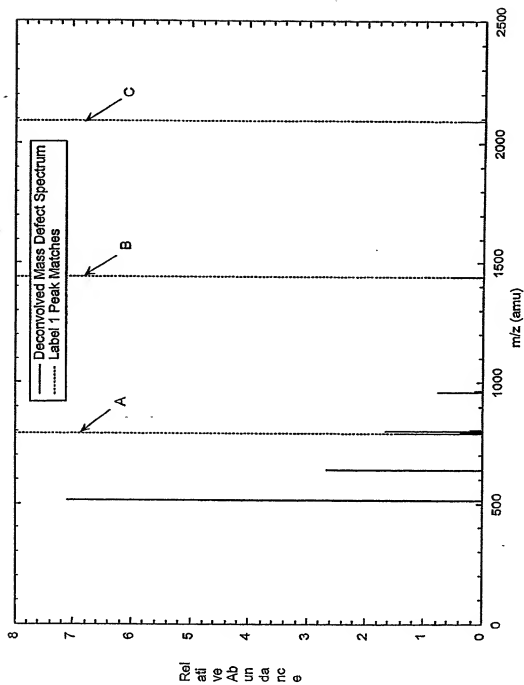


FIG. 21

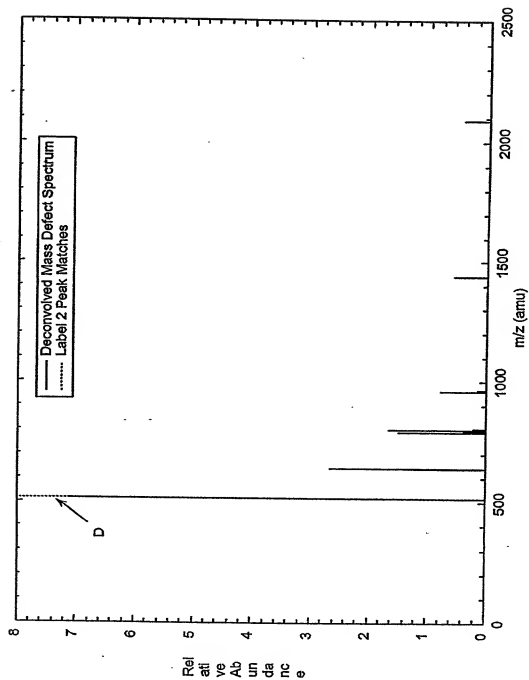


FIG. 22

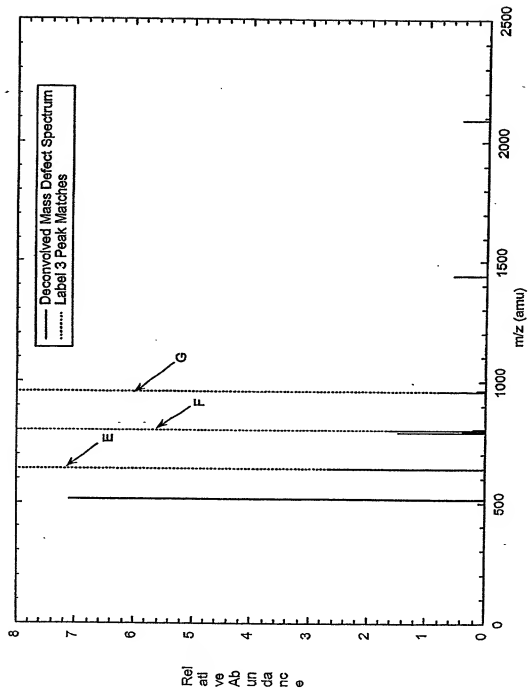


FIG. 2.3

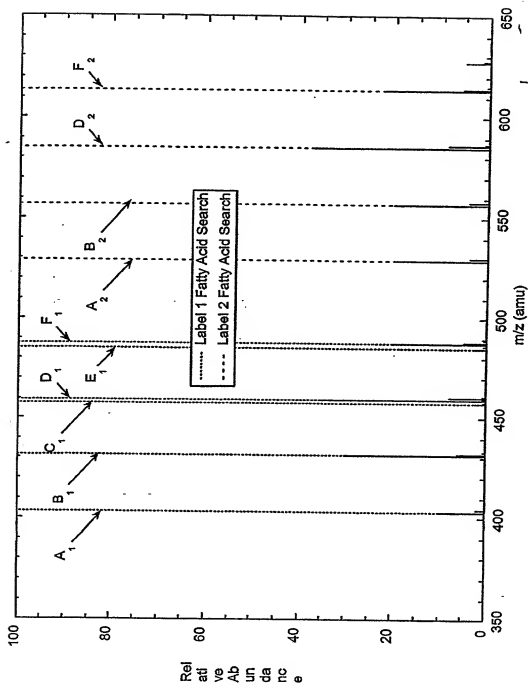
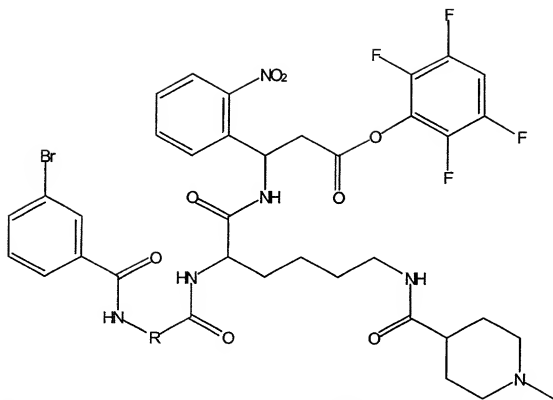


FIG. 2.4



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The general structure of the photocleavable mass defect tag where Br is the mass defect element that is linked through the amino acid (R) to the remainder of the tag.

FIG. 25

TOF MS E000001

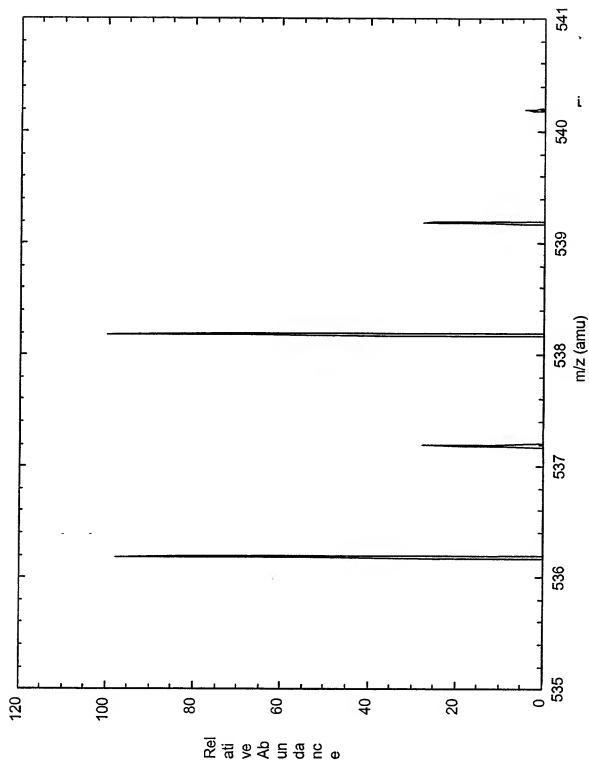


FIG 26

1061017-2022001

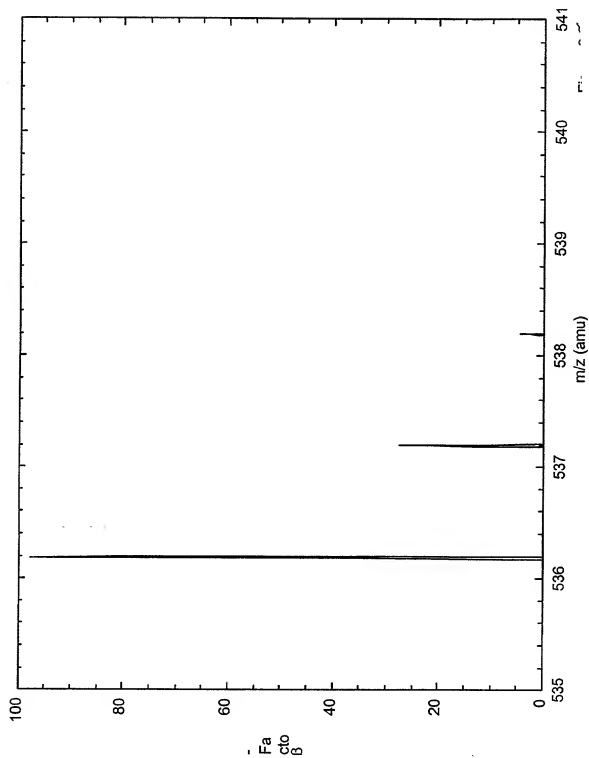


FIG 27

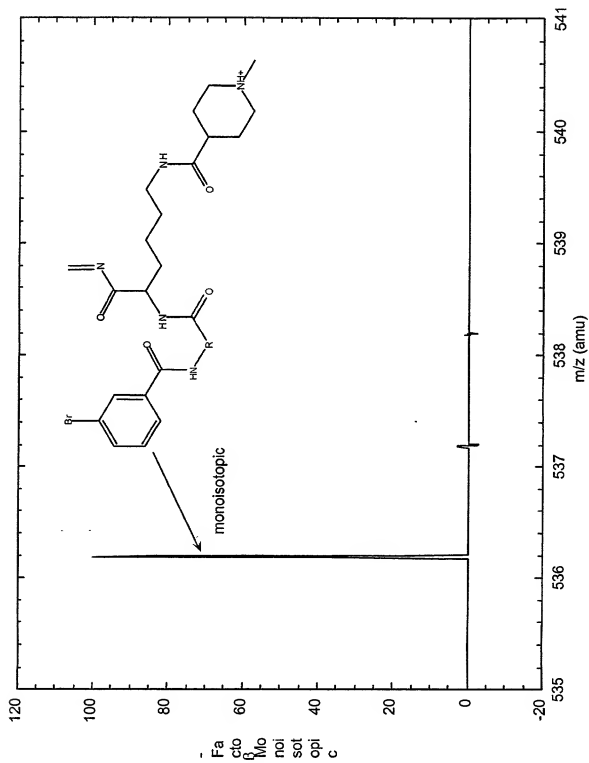


FIG 28

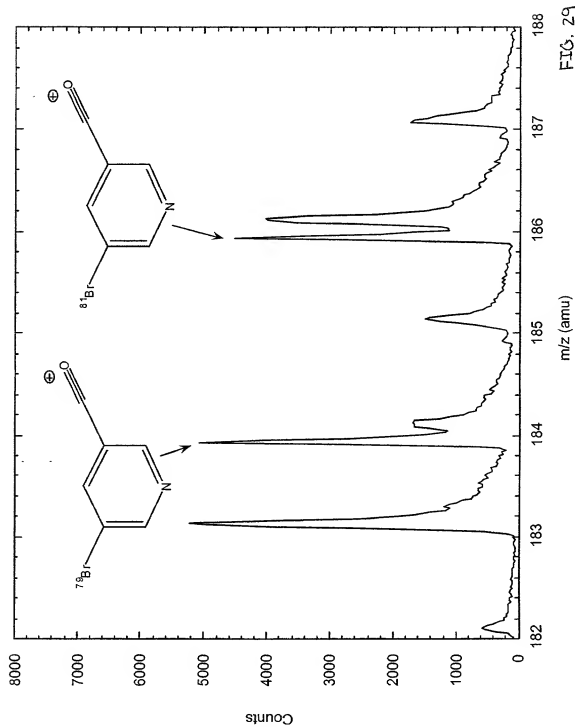


FIG. 29

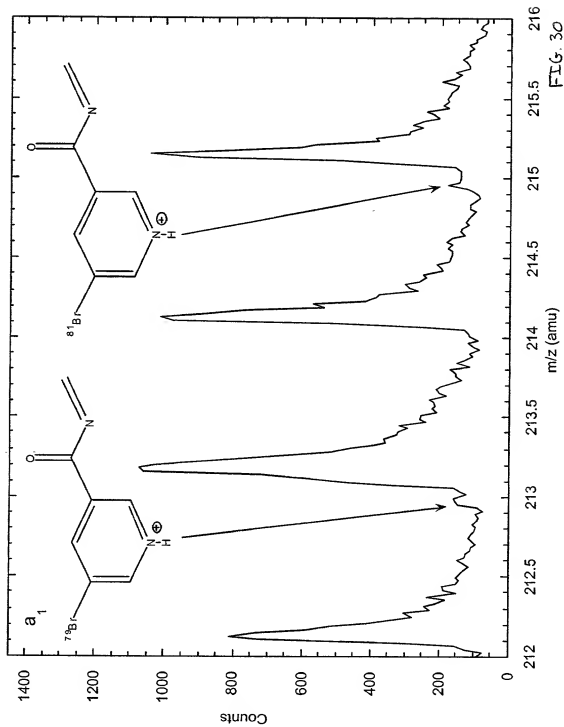


FIG. 30

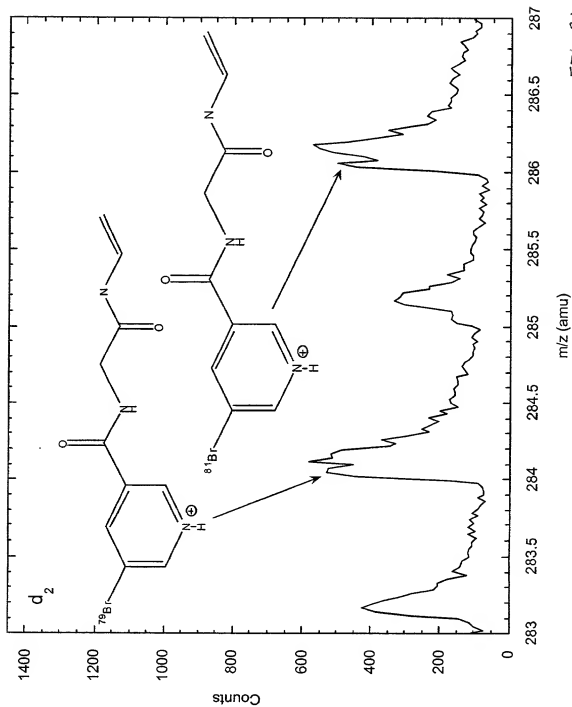
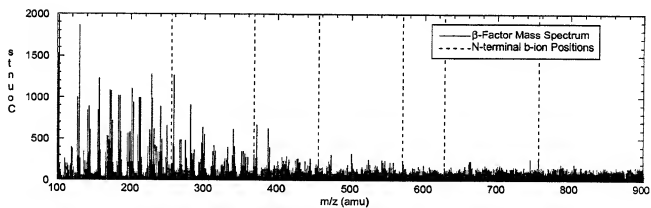
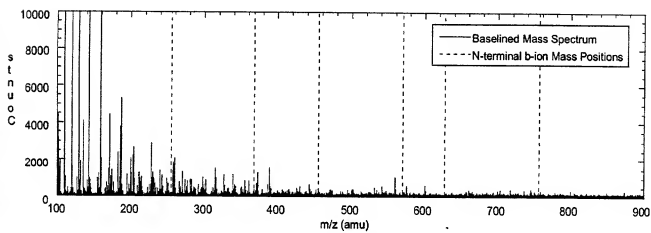
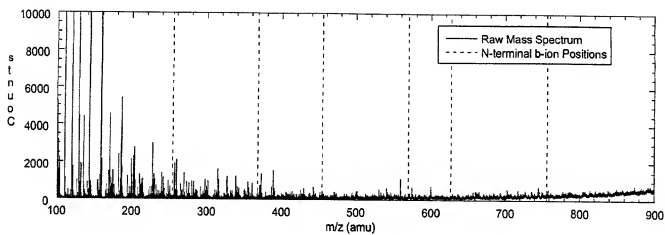


FIG. 31

Fig. 3.2



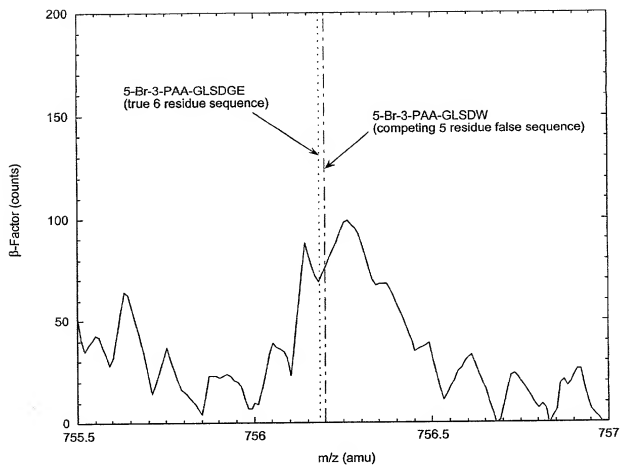


FIG. 33

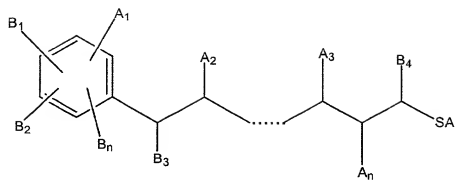


FIG. 34

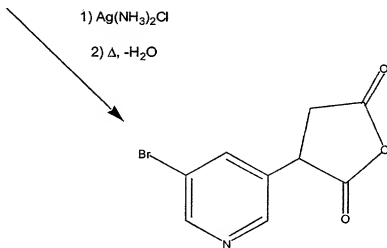
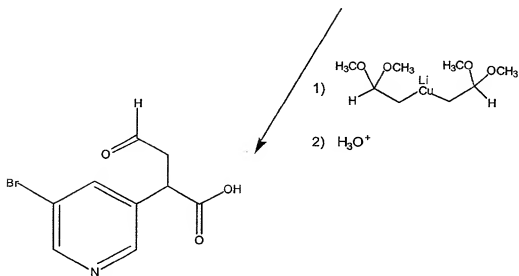
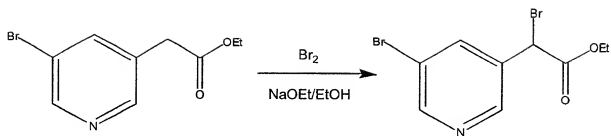


FIG. 35



M13 primer

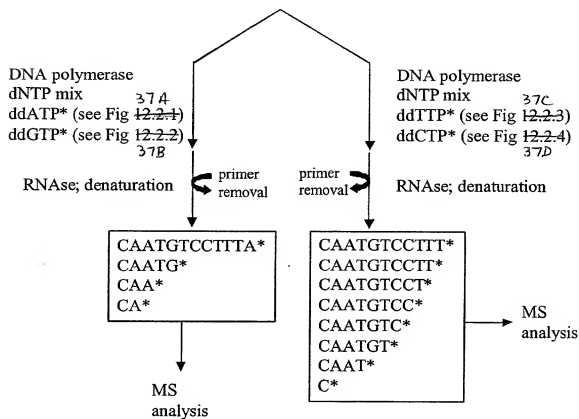
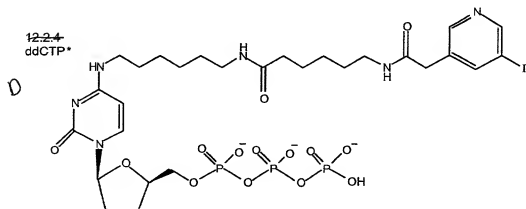
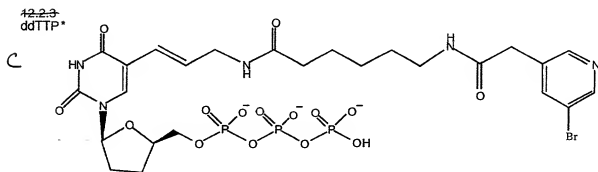
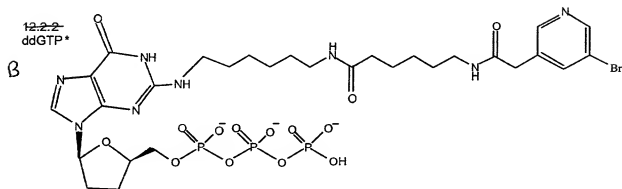
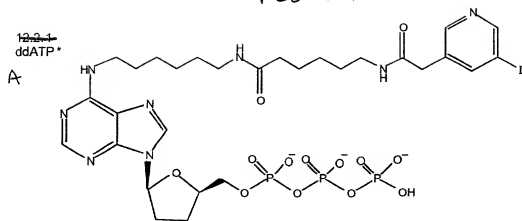


FIG. 36

FIG. 37



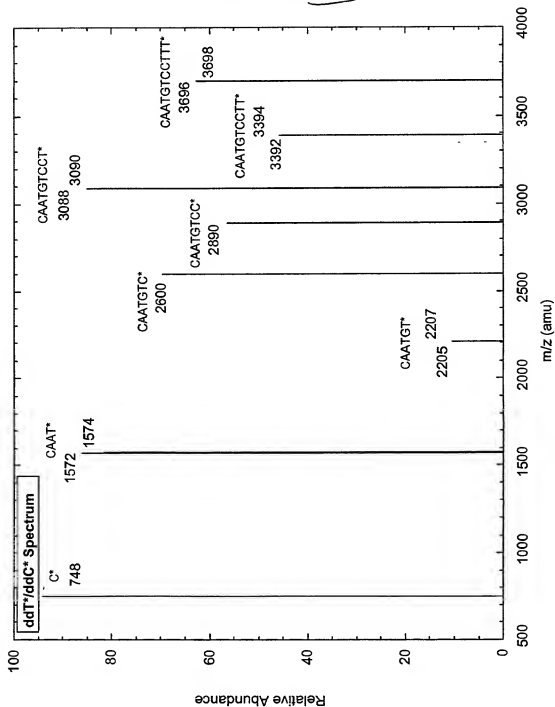


Fig. 39

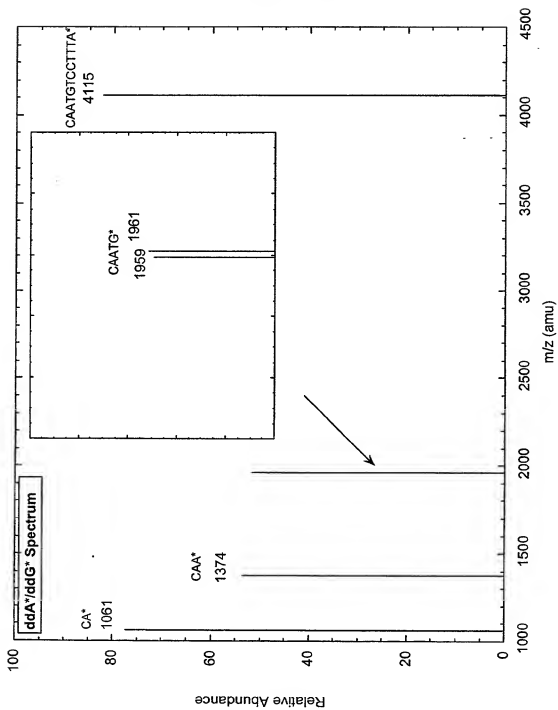


Fig. 38